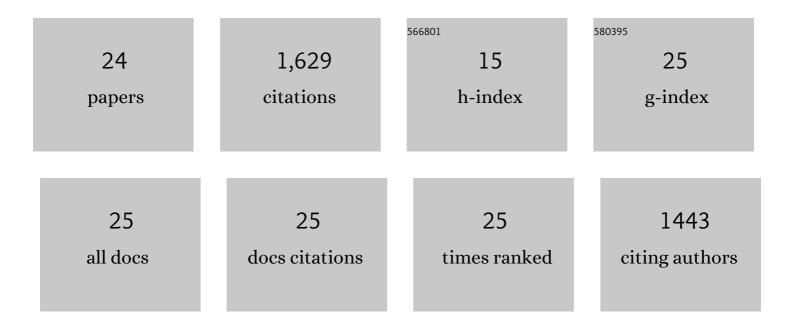
Satoshi Yamamoto

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Environmental DNA metabarcoding reveals local fish communities in a species-rich coastal sea. Scientific Reports, 2017, 7, 40368.	1.6	348
2	Environmental DNA as a â€~Snapshot' of Fish Distribution: A Case Study of Japanese Jack Mackerel in Maizuru Bay, Sea of Japan. PLoS ONE, 2016, 11, e0149786.	1.1	192
3	Effect of water temperature and fish biomass on environmental DNA shedding, degradation, and size distribution. Ecology and Evolution, 2019, 9, 1135-1146.	0.8	183
4	Rapid degradation of longer <scp>DNA</scp> fragments enables the improved estimation of distribution and biomass using environmental <scp>DNA</scp> . Molecular Ecology Resources, 2017, 17, e25-e33.	2.2	113
5	Dispersion and degradation of environmental DNA from caged fish in a marine environment. Fisheries Science, 2019, 85, 327-337.	0.7	102
6	An illustrated manual for environmental DNA research: Water sampling guidelines and experimental protocols. Environmental DNA, 2021, 3, 8-13.	3.1	102
7	Comparing local―and regionalâ€scale estimations of the diversity of stream fish using <scp>eDNA</scp> metabarcoding and conventional observation methods. Freshwater Biology, 2018, 63, 569-580.	1.2	88
8	Environmental DNA reflects spatial and temporal jellyfish distribution. PLoS ONE, 2017, 12, e0173073.	1.1	87
9	Sedimentary eDNA provides different information on timescale and fish species composition compared with aqueous eDNA. Environmental DNA, 2020, 2, 505-518.	3.1	77
10	Phylogeny of the Geometridae and the evolution of winter moths inferred from a simultaneous analysis of mitochondrial and nuclear genes. Molecular Phylogenetics and Evolution, 2007, 44, 711-723.	1.2	75
11	Incipient allochronic speciation by climatic disruption of the reproductive period. Proceedings of the Royal Society B: Biological Sciences, 2009, 276, 2711-2719.	1.2	51
12	Estimating fish population abundance by integrating quantitative data on environmental DNA and hydrodynamic modelling. Molecular Ecology, 2021, 30, 3057-3067.	2.0	50
13	Spatial Segregation and Aggregation of Ectomycorrhizal and Root-Endophytic Fungi in the Seedlings of Two Quercus Species. PLoS ONE, 2014, 9, e96363.	1.1	32
14	Parallel allochronic divergence in a winter moth due to disruption of reproductive period by winter harshness. Molecular Ecology, 2012, 21, 174-183.	2.0	22
15	Biomassâ€dependent emission of environmental DNA in jack mackerel <i>Trachurus japonicus</i> juveniles. Journal of Fish Biology, 2019, 95, 979-981.	0.7	18
16	Compilation of realâ€ŧime <scp>PCR</scp> conditions toward the standardization of <scp>environmental DNA</scp> methods. Ecological Research, 2021, 36, 379-388.	0.7	14
17	A generalist herbivore requires a wide array of plant species to maintain its populations. Biological Conservation, 2018, 228, 167-174.	1.9	13
18	Detection of herbivory: eDNA detection from feeding marks on leaves. Environmental DNA, 2020, 2, 627-634	3.1	13

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#	Article	IF	CITATIONS
19	eDNA as a tool for non-invasive monitoring of the fauna of a turbid, well-mixed system, the Elbe estuary in Germany. PLoS ONE, 2021, 16, e0250452.	1.1	12
20	Phylogenetic analysis of the winter geometrid genus Inurois reveals repeated reproductive season shifts. Molecular Phylogenetics and Evolution, 2016, 94, 47-54.	1.2	9
21	Estimations of Riverine Distribution, Abundance, and Biomass of Anguillid Eels in Japan and Taiwan Using Environmental DNA Analysis. Zoological Studies, 2020, 59, e17.	0.3	9
22	Characterizing the spatial and temporal occurrence patterns of the endangered botiid loach Parabotia curtus by environmental DNA analysis using a newly developed species-specific primer set. Ichthyological Research, 2021, 68, 152-157.	0.5	7
23	Environmental DNA emission by two carangid fishes in single and mixed-species tanks. Fisheries Science, 2022, 88, 55-62.	0.7	4
24	Population abundance gradient of Inurois punctigera along altitude. Entomological Science, 2020, 23, 23-27.	0.3	1